BIO392: CNV in cancer

Exploring Progenetix resource through R to investigate CNV pattern in cancer

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2023.09.27

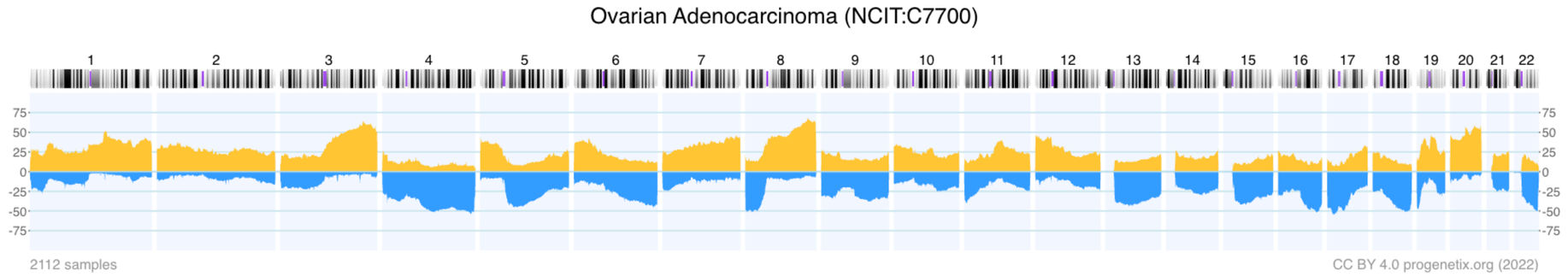
CNV frequency in Progenetix database

CNV frequency

Divide the genome into 1Mb-size bins and then count the occurrences of gain/loss events for all bins in the selected samples

Cancer genome data @ progenetix.org

The Progenetix database provides an overview of mutation data in cancer, with a focus on copy number abnormalities (CNV / CNA), for all types of human malignancies. The data is based on *individual sample data* from currently **142063** samples.



Download SVG | Go to NCIT:C7700 | Download CNV Frequencies

Example for aggregated CNV data in 2112 samples in Ovarian Adenocarcinoma.

Here the frequency of regional **copy number gains** and **losses** are displayed for all 22 autosomes.

Graded exercise

Upload .rmd file to GitHub course-result (deadline: 10.2 09:00am)

Glioblastoma

Invasive Breast Carcinoma

Lung Non-Small Cell Carcinoma

Colon Adenocarcinoma

Melanoma

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Requirement:
1. Could be rendered to .html file without error
2. Explain what the tumor you are studying is
3. Obtain the CNV frequency pattern of the tumor from Progenetix
4. Analyze:
- Which chromosomes have frequent gains and losses?
- Search the relevant literature to make a comparison.

pgxRpi package: https://github.com/progenetix/pgxRpi/